SEQUENCE LISTING

<110> FORSBERG, GORAN
ERLANDSSON, EVA
ANTONSSON, PER
WALSE, BJORN

<120> A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY

<130> P02188US0;10104199

<140> TBA
<141> 2001-06-20

<160> 7

<170> PatentIn version 3.0

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<211> 672
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<221> PEPTIDE
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<223> Conjugate protein

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1               5                  10                  15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30

Tyr Met His Trp Val Lys Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

Gly Arg Ile Asn Pro Asn Asn Gly Val Thr Leu Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Thr Met Ile Thr Asn Tyr Val Met Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
        115                 120                 125

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
    130                 135                 140

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
145                 150                 155                 160
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Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
            180                 185                 190

Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala
        195                 200                 205

Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Ser Gly Gly
    210                 215                 220

Pro Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys
225                 230                 235                 240

Ser Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr
                245                 250                 255

Tyr Asn Ser Lys Ala Ile Thr Ser Ser Glu Lys Ser Ala Asp Gln Phe
            260                 265                 270

Leu Thr Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp
        275                 280                 285

Tyr Asn Asp Leu Leu Val Asp Leu Gly Ser Thr Ala Ala Thr Ser Glu
    290                 295                 300

Tyr Glu Gly Ser Ser Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln
305                 310                 315                 320

Cys Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val
                325                 330                 335

Thr Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile
            340                 345                 350

Asn Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val
        355                 360                 365

Lys Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala
    370                 375                 380

Arg His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe
385                 390                 395                 400

Gly Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly
                405                 410                 415

Ser Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp
            420                 425                 430

Thr Leu Leu Arg Ile Tyr Arg Asp Asn Thr Thr Ile Ser Ser Thr Ser
        435                 440                 445

Leu Ser Ile Ser Leu Tyr Leu Tyr Thr Thr Ser Ile Val Met Thr Gln
    450                 455                 460

Thr Pro Thr Ser Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr
465                 470                 475                 480

Cys Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln
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485 490 495

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Tyr Thr Ser Ser Arg
500 505 510

Tyr Ala Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Tyr Gly Thr Asp
515 520 525

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Ala Ala Val Tyr
530 535 540

Phe Cys Gln Gln Asp Tyr Asn Ser Pro Pro Thr Phe Gly Gly Gly Thr
545 550 555 560

Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe
565 570 575

Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys
580 585 590

Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile
595 600 605

Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln
610 615 620

Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr
625 630 635 640

Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His
645 650 655

Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Ser
660 665 670

<210> 2
<211> 233
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<213> Artificial Sequence

<220>
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<400> 2

Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser
1 5 10 15

Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr
20 25 30

Asn Ser Lys Ala Ile Thr Ser Ser Glu Lys Ser Ala Asp Gln Phe Leu
35 40 45

Thr Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp Tyr
50 55 60

Asn Asp Leu Leu Val Asp Leu Gly Ser Thr Ala Ala Thr Ser Glu Tyr

65 70 75 80

Glu Gly Ser Ser Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys
85 90 95

Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
100 105 110

Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn
115 120 125

Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val Lys
130 135 140

Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
145 150 155 160

His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe Gly
165 170 175

Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly Ser
180 185 190

Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp Thr
195 200 205

Leu Leu Arg Ile Tyr Arg Asp Asn Thr Thr Ile Ser Ser Thr Ser Leu
210 215 220

Ser Ile Ser Leu Tyr Leu Tyr Thr Thr
225 230

<210> 3
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<221> peptide
<222> (1)..(233)
<223> Chimeric Protein

<400> 3

Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser
1 5 10 15

Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr
20 25 30

Asn Glu Lys Ala Ile Thr Glu Asn Lys Glu Ser Asp Asp Gln Phe Leu
35 40 45

Glu Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp Tyr
50 55 60

Asn Asp Leu Leu Val Asp Leu Gly Ser Lys Asp Ala Thr Asn Lys Tyr
65 70 75 80

Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys

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                85                  90                  95

Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
            100                 105                 110

Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn
        115                 120                 125

Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val Lys
    130                 135                 140

Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
145                 150                 155                 160

His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe Gly
                165                 170                 175

Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly Ser
            180                 185                 190

Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp Thr
        195                 200                 205

Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Leu
    210                 215                 220

His Ile Ala Leu Tyr Leu Tyr Thr Thr
225                 230

<210>  4
<211>  233
<212>  PRT
<213>  Staphylococcus sp.

<400>  4

Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser
1               5                   10                  15

Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr
            20                  25                  30

Asn Glu Lys Ala Lys Thr Glu Asn Lys Glu Ser His Asp Gln Phe Leu
        35                  40                  45

Gln His Thr Ile Leu Phe Lys Gly Phe Phe Thr Asp His Ser Trp Tyr
    50                  55                  60

Asn Asp Leu Leu Val Asp Phe Asp Ser Lys Asp Ile Val Asp Lys Tyr
65                  70                  75                  80

Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys
                85                  90                  95

Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
            100                 105                 110

Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn
        115                 120                 125

Leu Trp Leu Asp Gly Lys Gln Asn Thr Val Pro Leu Glu Thr Val Lys
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130 135 140

Thr Asn Lys Lys Asn Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
145 150 155 160

Arg Tyr Leu Gln Glu Lys Tyr Asn Leu Tyr Asn Ser Asp Val Phe Asp
165 170 175

Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Thr Ser Thr Glu Pro
180 185 190

Ser Val Asn Tyr Asp Leu Phe Gly Ala Gln Gly Gln Tyr Ser Asn Thr
195 200 205

Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Met
210 215 220

His Ile Asp Ile Tyr Leu Tyr Thr Ser
225 230

<210> 5
<211> 203
<212> PRT
<213> Staphylococcus sp.

<400> 5

Ala Leu His Lys Lys Ser Glu Leu Ser Ser Thr Ala Leu Asn Asn Met
1 5 10 15

Lys His Ser Tyr Ala Asp Ala Asn Pro Ile Ile Gly Ala Asn Lys Ser
20 25 30

Thr Gly Asp Gln Phe Leu Glu Asn Thr Leu Leu Tyr Lys Ala Phe Phe
35 40 45

Leu Leu Ile Asn Phe Asn Ser Ala Glu Met Ala Gln His Phe Lys Ser
50 55 60

Lys Asn Val Asp Val Tyr Ala Ile Arg Tyr Ala Ala Ala Cys Arg Thr
65 70 75 80

Ala Cys Thr Tyr Gly Gly Val Thr Pro His Ala Gly Asn Ala Leu Lys
85 90 95

Ala Arg Lys Lys Ile Pro Ile Asn Leu Trp Ile Ile Gly Val Gln Lys
100 105 110

Glu Val Ser Leu Asp Lys Val Gln Thr Asp Lys Lys Asn Val Thr Val
115 120 125

Gln Glu Leu Asp Ala Gln Ala Arg Arg Tyr Leu Gln Lys Asp Leu Lys
130 135 140

Leu Tyr Asn Ala Ile Gln Arg Gly Lys Leu Glu Phe Asp Ser Ala Ala
145 150 155 160

Ala Ser Lys Val Ser Tyr Asp Leu Phe Asp Val Ala Gly Asp Phe Pro
165 170 175

Glu Lys Gln Leu Arg Ile Tyr Ser Asp Asn Lys Thr Leu Ser Thr Glu

180 185 190

His Leu His Ile Asp Ile Tyr Leu Tyr Glu Ala
195 200

<210> 6
<211> 217
<212> PRT
<213> Staphylococcus sp.

<400> 6

Glu Asp Leu His Asp Lys Ser Glu Leu Thr Asp Leu Ala Leu Ala Asn
1 5 10 15

Ala Tyr Gly Gln Tyr Asn His Pro Phe Ile Lys Glu Asn Ile Lys Ser
20 25 30

Asp Glu Ile Ser Gly Glu Lys Asp Leu Ile Phe Arg Asn Gln Gly Asp
35 40 45

Ser Gly Asn Asp Leu Arg Val Lys Phe Ala Thr Ala Asp Leu Ala Gln
50 55 60

Lys Phe Lys Asn Lys Asn Val Asp Ile Tyr Gly Ala Ser Phe Tyr Tyr
65 70 75 80

Lys Cys Glu Lys Ile Ser Glu Asn Ile Ser Glu Cys Leu Tyr Gly Gly
85 90 95

Thr Thr Leu Asn Ser Glu Lys Leu Ala Gln Glu Arg Val Ile Gly Ala
100 105 110

Asn Val Trp Val Asp Gly Ile Gln Lys Glu Thr Glu Leu Ile Arg Thr
115 120 125

Asn Lys Lys Asn Val Thr Leu Gln Glu Leu Asp Ile Lys Ile Arg Lys
130 135 140

Ile Leu Ser Asp Lys Tyr Lys Ile Tyr Tyr Lys Asp Ser Glu Ile Ser
145 150 155 160

Lys Gly Leu Ile Glu Phe Asp Met Lys Thr Pro Arg Asp Tyr Ser Phe
165 170 175

Asp Ile Tyr Asp Leu Lys Gly Glu Asn Asp Tyr Glu Ile Asp Lys Ile
180 185 190

Tyr Glu Asp Asn Lys Thr Leu Lys Ser Asp Asp Ile Ser His Ile Asp
195 200 205

Val Asn Leu Tyr Thr Lys Lys Lys Val
210 215

<210> 7
<211> 233
<212> PRT
<213> Staphylococcus sp.

<400> 7

Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser
1 5 10 15

Glu Leu Gln Arg Asn Ala Leu Ser Asn Leu Arg Gln Ile Tyr Tyr Tyr
20 25 30

Asn Glu Lys Ala Ile Thr Glu Asn Lys Glu Ser Asp Asp Gln Phe Leu
35 40 45

Glu Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp Tyr
50 55 60

Asn Asp Leu Leu Val Asp Leu Gly Ser Lys Asp Ala Thr Asn Lys Tyr
65 70 75 80

Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys
85 90 95

Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
100 105 110

Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn
115 120 125

Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val Lys
130 135 140

Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
145 150 155 160

His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe Gly
165 170 175

Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly Ser
180 185 190

Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp Thr
195 200 205

Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Leu
210 215 220

His Ile Asp Leu Tyr Leu Tyr Thr Thr
225 230